

Sequence

; GAP of: W0h051-7.Seq check: 6926 from: 1 to: 52

seq of dicamba induced band w0c0 51.7

to: Cjlp181r.Seq check: 2737 from: 1 to: 714

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	520	Length:	714
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

W0h051-7.Seq x Cjlp181r.Seq..

1gctagctgcgccgtgaccacgcacat	26
1	CGATCGAAGTGGGTGTGTCAGCTAGCTAGCTGCGCCGTGACCAACGCACAT	50
	
27	gaccgcagtcgcgcgggctgatca.....	52
51	GACCGCAGTGC GCGCGGGGCTGATCAAGGAAAGTATCGGATGGAGCTG	100

Figure 2

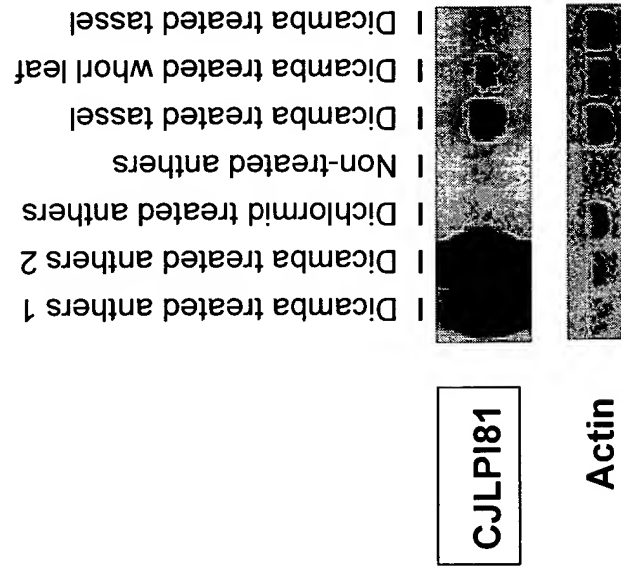


Figure 3

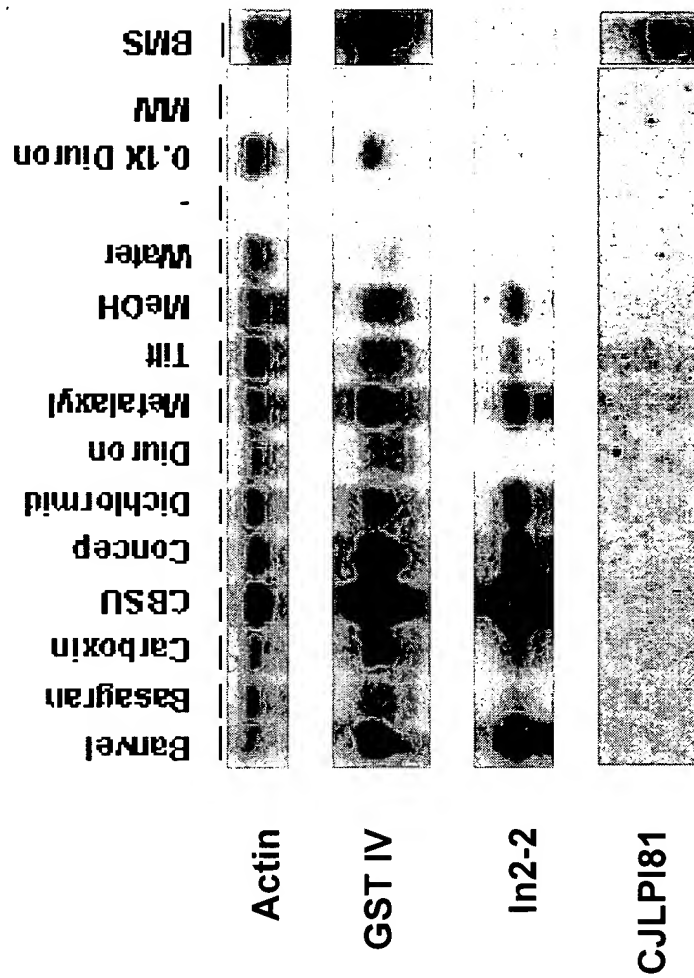


Figure 4

[illegible]

ZmAxig1 PS-IAA4/5

```
DOMAIN I . . . NLS .
1 MELELGLAPPNP HQPLAAAAEFVGLSSAGSCGNKRVLGDAFGAAKAAT 50
||| ||| : | : || : |||
mefkate lrlgl.pg.....iteeeekiihgssvvnknkr..... 36

. . . DOMAIN II. NLS .
51 LPLFVCEDGDGGDDRDRDGVVDHEQQSNNVPRKKRLVGWPPVKARRRS 100
| : | : | | | : ||| : | : |
qlptseesvsiskvtndehi.vesssaappakakivgwppirsyrkns 84

. . . DOMAIN III . . .
101 .....CGGYVKVKLEGVPIGRKVDVSIHGSYOELLRTLESMPSGNQOD 145
|| : ||| :: | | | : | | | : | | | :
lheadvgg ifvkvsmdgapylrkidlrvyggysellkaletmfkl.tige 133

      β          α
. . . . DOMAIN IV. NLS .
146 HADEVVVSHERRRRHPYVVTYEDGEDWLLVGDDVPWEVFVKSVKRLKI 195
:: | | | | | | | : ||| : | | | : | | | : |
yseregykgse.....yaptyedkdgdwmvlvg.dvpwdmfvtscrlri 176

.
196 LA..... 197
:
177 mkgteakglgcgv 189
```

Figure 5

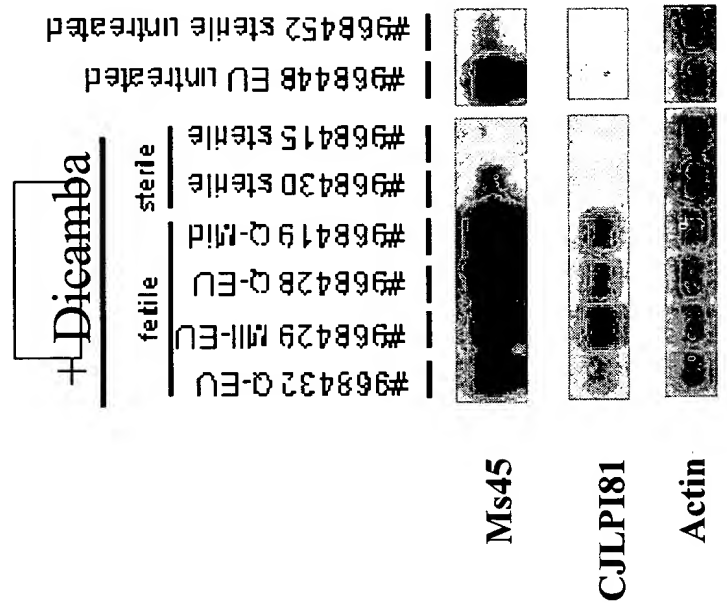


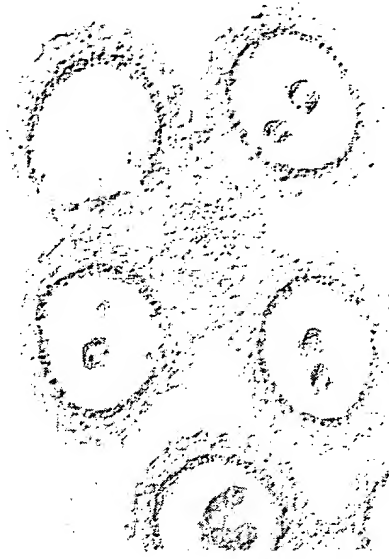
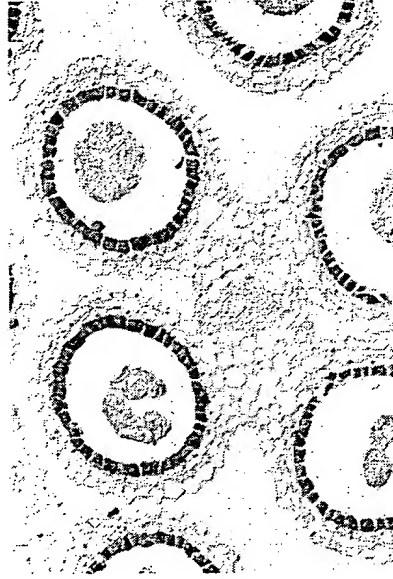
Figure 6

[illegible]

+ Dicamba

-Dicamba

Axig1 antisense probe



Axigl sense probe

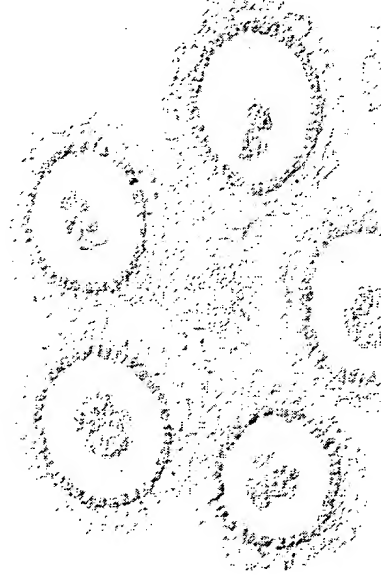


Figure 7

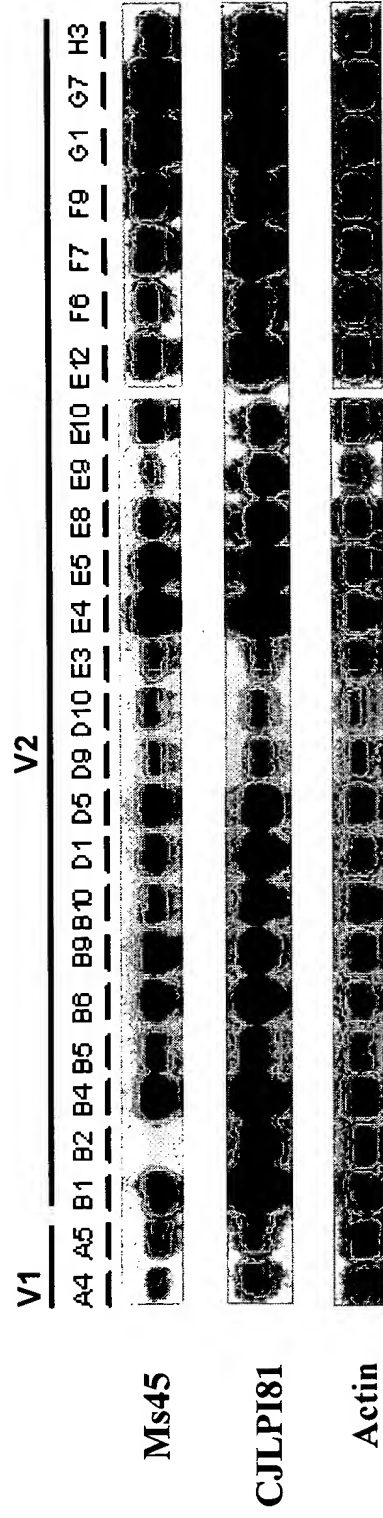


Figure 8

Figure 9

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

Symbol comparison table:
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 10871 Length: 3123
Ratio: 8.955 Gaps: 3
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ..

```

      . . . . .
1 .....GCAGGAACTTAT 12
      |||||
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAACTTAT 1150
      .
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
      |||||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
      .
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 112
      |||||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTTCAGCTAGCTAGCTGCG 1250
      .
113 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 162
      |||||
1251 CCGTGACCACGCACATGACCGCAGTGCGCGCGGGGCTGATCAAGGGAAAG 1300
      .
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
      |||||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
      .
213 CGCTGGCTGCCGCCGCCGAGTTCGTCTCGGTCTCCTCAGCAGCTCGGCTGGC 262
      |||||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTCTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
      .
263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
      |||||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
      .
313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
      |||||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500
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790 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
 ||||||||||||||||||||||||||||||||||||||||
 2301 GTGTGGTCCGTCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350
 840 TCTGCGTAATAACGTTGTTTCTGTCTGTGTGCCCCGTAGCAGTACGTACT 889
 ||||||||||||||||||||||||||||||||||||||||
 2351 TCTGCGTAATAACGTTGTTTCTGTCTGTGTGCCCCGTAGCAGTACGTACT 2400
 890 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTTCAGAGCATGAC 939
 ||||||||||||||||||||||||||||||||||||||||
 2401 GTCCTATAGTAAGCTAGCTTTATGGGGTGCTTCAGCTTTTCAGAGCATGAC 2450
 940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 989
 ||||||||||||||||||||||||||||||||||||||||
 2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCGT 2500
 990 ACGGTATCGCTGGCGTCAGTGTGCGGCAGCCTAGGTGATCTAAGCATAC 1039
 ||||||||||||||||||||||||||||||||||||||||
 2501 ACGGTATCGCTGGCGTCAGTGTGCGGCAGCCTAGGTGATCTAAGCATAC 2550
 1040 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 1089
 ||||||||||||||||||||||||||||||||||||||||
 2551 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCATGGTAATTCATA 2600
 1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 1139
 ||||||||||||||||||||||||||||||||||||||||
 2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCTTAAGGCACAGGGG 2650
 1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 1189
 ||||||||||||||||||||||||||||||||||||||||
 2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATAACTATTTAAC 2700
 1190 ACTGTTTCATCAATATATTTGATTTT..... 1214
 ||||||||||||||||||||||||
 2701 ACTGTTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sequence Name	SEQ ID NO:	ATCC Deposit
Pioneer clone CZAAL47	1	PTA-2426
ZmAxig1 polypeptide	2	
Native ZmAxig1 promoter region	3	
Modified ZmAxig1 promoter region	4	PTA-2427
A632 full-length ZmAxig1, including SEQ ID No. 3	5	PTA-2426 PTA-2427
Primer 1, used for isolation of 5' flanking region	6	
Primer 2, used for isolation of 5' flanking region	7	
Primer 3, used for isolation of region spanning start codon	8	
Primer 4, used for isolation of region spanning start codon	9	
Primer 5, used for isolation of 5' region	10	
Oligonucleotide designed to remove clones having a poly-A tail but no cDNA	11	
Pioneer clone Cjlp181	12	
CuraGen fragment w0h051.7	13	
Primer 6, used to isolate the coding sequence and 3' region	14	
Primer 7, used to isolate the coding sequence and 3' region	15	
Modified ZmAxig1 promoter region with single-base deletion	16	PTA-2427
LEC1 transcriptional activator element	17	
LEC1 polynucleotides	18-20	
LEC1 polypeptide consensus sequence	21	

Figure 10. Representative polynucleotides and polypeptides of the present invention.

Experiment	Control	Ubi:LEC1	Axig1:LEC1
#1 3938.37	15%	63%	44%
#2 3938.79	4%	17%	20%
#3 3938.78	16%	17%	38%
#4 3938.34	2%	14%	13%

Figure 11. Transformation frequencies by LEC1 with two different promoters. Transformation frequencies were based on the percentage of plated embryos with one or more GFP positive/Bialaphos resistant colonies. All embryos were shot with Ubi:moPAT~GFP (a construct conferring Bialaphos resistance and GFP fluorescence) along with a LEC1 construct or a control DNA.